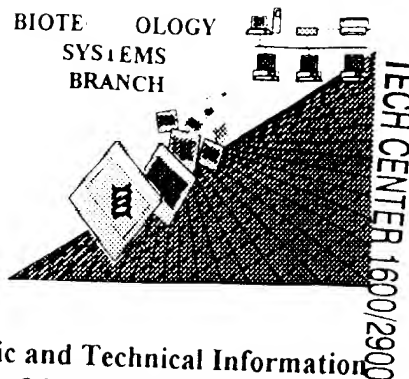


RAW SEQUENCE LISTING
ERROR REPORT



AUG 31 2001

RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09 518156

Source: AU 1645

Date Processed by STIC: 08/06/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Does Not Comply
Corrected Diskette Needed

1645

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

3 <110> APPLICANT: Tarleton, Rick
 4 Garg, Nisha
 6 <120> TITLE OF INVENTION: PROPHYLACTIC AND THERAPEUTIC IMMUNIZATION AGAINST INFECTION
 AND DISEASE
 8 <130> FILE REFERENCE: 235.00201010
 10 <140> CURRENT APPLICATION NUMBER: 09/518,156
 11 <141> CURRENT FILING DATE: 2000-03-02
 13 <150> PRIOR APPLICATION NUMBER: 60/122,532
 14 <151> PRIOR FILING DATE: 1999-03-02
 16 <160> NUMBER OF SEQ ID NOS: 24
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 8
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Trypanosoma cruzi
 25 <400> SEQUENCE: 1
 27 Val Asp Tyr Asn Phe Thr Ile Val
 28 1 5
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 8
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Gallus gallus
 35 <400> SEQUENCE: 2
 37 Ser Ile Ile Asn Phe Glu Lys Leu
 38 1 5
 40 <210> SEQ ID NO: 3
 41 <211> LENGTH: 34
 42 <212> TYPE: DNA
 C--> 43 <213> ORGANISM: Artificial
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: forward primer
 48 <400> SEQUENCE: 3
 49 agtcgacgga tccatgattg catttgctga aggc
 52 <210> SEQ ID NO: 4 34
 53 <211> LENGTH: 35
 54 <212> TYPE: DNA
 C--> 55 <213> ORGANISM: Artificial
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: reverse primer
 60 <400> SEQUENCE: 4
 61 atctagaagc ttcatagttc accgacactc agtgg
 64 <210> SEQ ID NO: 5 35
 65 <211> LENGTH: 35
 66 <212> TYPE: DNA
 C--> 67 <213> ORGANISM: Artificial
 69 <220> FEATURE:
 70 <223> OTHER INFORMATION: reverse primer
 72 <400> SEQUENCE: 5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

73 atctagaagc ttcattgccgc agcatttgct tcccc
 76 <210> SEQ ID NO: 6.
 77 <211> LENGTH: 0
 78 <212> TYPE: PRT
 79 <213> ORGANISM: ~~Skipped Sequence~~
 81 <400> SEQUENCE: 6

W--> 82 000
 84 <210> SEQ ID NO: 7
 85 <211> LENGTH: 8
 86 <212> TYPE: PRT
 87 <213> ORGANISM: Trypanosoma cruzi
 89 <400> SEQUENCE: 7
 91 Val Asn His Arg Phe Thr Leu Val
 92 1 5
 94 <210> SEQ ID NO: 8
 95 <211> LENGTH: 8
 96 <212> TYPE: PRT
 97 <213> ORGANISM: Trypanosoma cruzi
 99 <400> SEQUENCE: 8
 101 Val Asn His Asp Phe Thr Val Val
 102 1 5
 104 <210> SEQ ID NO: 9
 105 <211> LENGTH: 0
 106 <212> TYPE: PRT
 107 <213> ORGANISM: ~~Skipped Sequence~~
 109 <400> SEQUENCE: 9

W--> 110 000
 112 <210> SEQ ID NO: 10
 113 <211> LENGTH: 28
 114 <212> TYPE: DNA
 C--> 115 <213> ORGANISM: Artificial
 117 <220> FEATURE:
 118 <223> OTHER INFORMATION: forward primer
 120 <400> SEQUENCE: 10
 121 aggatccatg attgcatttg tcgaaggc
 124 <210> SEQ ID NO: 11
 125 <211> LENGTH: 30
 126 <212> TYPE: DNA
 C--> 127 <213> ORGANISM: Artificial
 129 <220> FEATURE:
 130 <223> OTHER INFORMATION: reverse primer
 132 <400> SEQUENCE: 11
 133 aaagcttcac agttcaccga cactcagtgg
 136 <210> SEQ ID NO: 12
 137 <211> LENGTH: 26
 138 <212> TYPE: DNA
 C--> 139 <213> ORGANISM: Artificial
 141 <220> FEATURE:
 142 <223> OTHER INFORMATION: forward primer

Errors
 When a sequence is skipped
 only fields 210 and 400 are
 included. *mt*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

```

144 <400> SEQUENCE: 12
145 aagatcttgt ggaaaggaat ttgagg
148 <210> SEQ ID NO: 13
149 <211> LENGTH: 28
150 <212> TYPE: DNA
C--> 151 <213> ORGANISM: Artificial
153 <220> FEATURE:
154 <223> OTHER INFORMATION: reverse primer
156 <400> SEQUENCE: 13
157 actcgagtca cagtgggcgg ttgtacag
160 <210> SEQ ID NO: 14
161 <211> LENGTH: 27
162 <212> TYPE: DNA
C--> 163 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: forward primer
168 <400> SEQUENCE: 14
169 aagatctctg tgaggctgca gacgctg
172 <210> SEQ ID NO: 15
173 <211> LENGTH: 28
174 <212> TYPE: DNA
C--> 175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: reverse primer
180 <400> SEQUENCE: 15
181 acccggggta ttggtcgcca ccgtttcc
184 <210> SEQ ID NO: 16
185 <211> LENGTH: 26
186 <212> TYPE: DNA
C--> 187 <213> ORGANISM: Artificial
189 <220> FEATURE:
190 <223> OTHER INFORMATION: forward primer
192 <400> SEQUENCE: 16
193 ggttcgattg gggttggtgt aatata
196 <210> SEQ ID NO: 17
197 <211> LENGTH: 26
198 <212> TYPE: DNA
C--> 199 <213> ORGANISM: Artificial
201 <220> FEATURE:
202 <223> OTHER INFORMATION: reverse primer
204 <400> SEQUENCE: 17
205 aaataatgta cgggkgagat gcatga
208 <210> SEQ ID NO: 18
209 <211> LENGTH: 0
210 <212> TYPE: DNA
211 <213> ORGANISM: Skipped Sequence
213 <400> SEQUENCE: 18
W--> 214 000
216 <210> SEQ ID NO: 19

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

```

217 <211> LENGTH: 0
218 <212> TYPE: DNA
219 <213> ORGANISM: Skipped Sequence
221 <400> SEQUENCE: 19
W--> 222 000
224 <210> SEQ ID NO: 20
225 <211> LENGTH: 1656
226 <212> TYPE: DNA
227 <213> ORGANISM: Trypanosoma cruzi
229 <400> SEQUENCE: 20
230 atgcggaaga aagccgcagc attagcagcg cccacagcag acacacggcc gacgtgccgc 60
232 ggggctgccca ttgccaatata atttatggaa cgtgccggcc cccgtgaggg cgttgggaga 120
234 tcaacggaga tgccggctgc tggaccgacg ggggtctcaa gaactcaaac gcaacgggag 180
236 gtgaaagcgt cacaagacgc cgacgcggcg gccattagta gttatttcca gtccgaattg 240
238 gtgacatctc agtcgcacga ggggtgtgtct cctctggcaa agactagggc caacgaacgg 300
240 cggaacgggg agcaggagcg ggagaaggaa ctgccggcgg ttggtggcgc cgttccaact 360
242 ggggaagggga cggaccccaa acagcgagtg ctgcaggatt tgccagcgat gcacgcggag 420
244 ggacaaaacc agcacggtag agaggggtgac aagggtgttt ccgtgaagat ggactcccct 480
246 ggtcgcgtac aggtgctgga gcaaattgtt ctacacctgg ctgcattgaa cagacagcta 540
248 gaattagaac ttatagaaac ggcacgggaa ctgacgatgt acaagcagct tttacctgat 600
250 gtgcagcgcc agaccgagcg ccatgctttg tctcaggagc atcacaagc gaatagtgtc 660
252 gctccgccac tgatgtcaga tgagaggcga cgacagatgc tctttacagg gcaacaacaa 720
254 caacagcaac aagtgggaaga tctgcatggc ggtattagcg ggtgggaaac ggcagcgagg 780
256 agaattgcgt atggttacga ggagggggag agggacgccc ttccagatgg tgagggccgt 840
258 ccacgttgcg caggtcgtat gggctccccg aagagattcc tttcaacaca accgcctcga 900
260 agcagcagga accatcgga cctcacgct gctaacggga caaatggcaa tagtcatgtt 960
262 ccccatctct ccagacaaaa aagtcacccg acaagaggag ctgctgtaac ttccgtaccg 1020
264 ttggcgcgct ccgcaaccaa tcgccgaggt cgttccatgc gacaacatac ccgacccgcg 1080
266 ggaccttctt atcttttcga acgcctcgac gctgaggatg caattgatat gctggagacg 1140
268 ctgaagcgct ctctcatgta tcgctgcaac cactcgcatc atcgatcaac agaaggagat 1200
270 gttgtgcggc ccgcgcgcga gcccgggaaa ggcacgcggt ctgttccacc accaccgcca 1260
272 ccaccgcccc tgtcatcatc gtcacaaaga aagcttgccg ccgcagttgc tggagcgccg 1320
274 gcatgcagcg tctcagcagc acacggaagg aaccatggcg tttctgcggt gggagatccg 1380
276 tcaaggggca atcgagtttc agaaacagct cgcatagctc atgctccttc ttttgggggg 1440
278 aagaaatgcg cgccgggcct aacccaactc catctctctt ccccttcag aagggctacg 1500
280 ccgatgaaaa aagacacgcc attgtcacgt ggtcaagcgg ctggagtagc agcagtagcg 1560
282 gtgggcggtg acgggcagct agaggcactg cagagggcgtt actgggaaca gtcccgtgcg 1620
284 atattggagc agcttgaaaa catgctggca gctgat 1656
287 <210> SEQ ID NO: 21
288 <211> LENGTH: 39
289 <212> TYPE: DNA
C--> 290 <213> ORGANISM: Artificial
292 <220> FEATURE:
293 <223> OTHER INFORMATION: pTAT linker ✓
295 <400> SEQUENCE: 21
296 tccaccatgg ccggtaccgg tctcgaggtg catgcggtg 39
299 <210> SEQ ID NO: 22
300 <211> LENGTH: 14
301 <212> TYPE: PRT

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:53

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

C--> 302 <213> ORGANISM: Artificial

304 <220> FEATURE:

305 <223> OTHER INFORMATION: pTAT linker

307 <400> SEQUENCE: 22

309 Gly Ser Thr Met Ala Gly Thr Gly Leu Glu Val His Ala Val
310 1 5 10

312 <210> SEQ ID NO: 23

313 <211> LENGTH: 41

314 <212> TYPE: DNA

C--> 315 <213> ORGANISM: Artificial

317 <220> FEATURE:

318 <223> OTHER INFORMATION: pTAT-HA linker

320 <400> SEQUENCE: 23

321 ccatgtccgg ctatccatat gacgtcccag actatgctgg c

324 <210> SEQ ID NO: 24

325 <211> LENGTH: 13

326 <212> TYPE: PRT

41

C--> 327 <213> ORGANISM: Artificial

329 <220> FEATURE:

330 <223> OTHER INFORMATION: pTAT-HA linker

332 <400> SEQUENCE: 24

334 Met Ser Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
335 1 5 10

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/518,156

DATE: 08/06/2001

TIME: 15:04:54

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF3\08062001\I518156.raw

L:43 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:55 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:67 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:82 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:110 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:115 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:127 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:139 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:151 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:163 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:175 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:187 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:199 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:214 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:222 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:290 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:302 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:315 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:327 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/513,196
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input checked="" type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	